

D.Krose

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*[Handwritten signature]*



1638

RAW SEQUENCE LISTING

DATE: 05/21/2002

PATENT APPLICATION: US/09/697,719

TIME: 13:32:37

Input Set : A:\0020-4764P.st25A.txt

Output Set: N:\CRF3\05212002\I697719.raw

P.6

3 <110> APPLICANT: NAKAJIMA, Hiroki  
4 NAGASAWA, Akitsu  
6 <120> TITLE OF INVENTION: Method for giving resistance to weed control compounds to  
plants  
8 <130> FILE REFERENCE: 0020-4764P  
10 <140> CURRENT APPLICATION NUMBER: 09/697,719  
11 <141> CURRENT FILING DATE: 2000-10-27  
13 <150> PRIOR APPLICATION NUMBER: JP 10/120553  
14 <151> PRIOR FILING DATE: 1998-04-30  
16 <150> PRIOR APPLICATION NUMBER: JP 10/281127  
17 <151> PRIOR FILING DATE: 1998-10-02  
19 <150> PRIOR APPLICATION NUMBER: JP 10/330981  
20 <151> PRIOR FILING DATE: 1998-11-20  
22 <150> PRIOR APPLICATION NUMBER: JP 11/054730  
23 <151> PRIOR FILING DATE: 1999-03-02  
25 <160> NUMBER OF SEQ ID NOS: 78  
27 <210> SEQ ID NO: 1  
28 <211> LENGTH: 39  
29 <212> TYPE: DNA  
30 <213> ORGANISM: Artificial Sequence  
32 <220> FEATURE:  
33 <223> OTHER INFORMATION: Designed oligonucleotide primer to amplify bchH gene  
35 <400> SEQUENCE: 1  
36 gacatctaga ggagacgacc atatgcacgg tgaagtctc 39  
38 <210> SEQ ID NO: 2  
39 <211> LENGTH: 31  
40 <212> TYPE: DNA  
41 <213> ORGANISM: Artificial Sequence  
43 <220> FEATURE:  
44 <223> OTHER INFORMATION: Designed oligonucleotide primer to amplify bchH gene  
46 <400> SEQUENCE: 2  
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49 <210> SEQ ID NO: 3  
50 <211> LENGTH: 39  
51 <212> TYPE: DNA  
52 <213> ORGANISM: Artificial Sequence  
54 <220> FEATURE:  
55 <223> OTHER INFORMATION: Designed oligonucleotide primer to amplify soybean PPO gene  
57 <400> SEQUENCE: 3  
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60 <210> SEQ ID NO: 4  
61 <211> LENGTH: 36  
62 <212> TYPE: DNA  
63 <213> ORGANISM: Artificial Sequence

ENTERED

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65 &lt;220&gt; FEATURE:

66 &lt;223&gt; OTHER INFORMATION: Designed oligonucleotide primer to amplify soybean PPO gene

68 &lt;400&gt; SEQUENCE: 4

69 ttgtcgacaa ctgctactat ttgtacactc tatttg 36

71 &lt;210&gt; SEQ ID NO: 5

72 &lt;211&gt; LENGTH: 1632

73 &lt;212&gt; TYPE: DNA

74 &lt;213&gt; ORGANISM: Glycine max var. Williams82

76 &lt;220&gt; FEATURE:

77 &lt;221&gt; NAME/KEY: CDS

78 &lt;222&gt; LOCATION: (1)...(1632)

80 &lt;400&gt; SEQUENCE: 5

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82 Met Val Ser Val Phe Asn Glu Ile Leu Phe Pro Pro Asn Gln Thr Leu

83 1 5 10 15

84 ctt cgc ccc tcc ctc cat tcc cca acc tct ttc ttc acc tct ccc act 96

85 Leu Arg Pro Ser Leu His Ser Pro Thr Ser Phe Phe Thr Ser Pro Thr

86 20 25 30

87 cga aaa ttc cct cgc tct cgc cct aac cct att cta cgc tgc tcc att 144

88 Arg Lys Phe Pro Arg Ser Arg Pro Asn Pro Ile Leu Arg Cys Ser Ile

89 35 40 45

90 gcg gag gaa tcc acc gcg tct ccg ccc aaa acc aga gac tcc gcc ccc 192

91 Ala Glu Glu Ser Thr Ala Ser Pro Pro Lys Thr Arg Asp Ser Ala Pro

92 50 55 60

93 gtg gac tgc gtc gtc gtc ggc gga ggc gtc agc ggc ctc tgc atc gcc 240

94 Val Asp Cys Val Val Val Gly Gly Gly Val Ser Gly Leu Cys Ile Ala

95 65 70 75 80

96 cag gcc ctc gcc acc aaa cac gcc aat gcc aac gtc gtc gtc acg gag 288

97 Gln Ala Leu Ala Thr Lys His Ala Asn Ala Asn Val Val Val Thr Glu

98 85 90 95

99 gcc cga gac cgc gtc ggc ggc aac atc acc acg atg gag agg gac gga 336

100 Ala Arg Asp Arg Val Gly Gly Asn Ile Thr Thr Met Glu Arg Asp Gly

101 100 105 110

102 tac ctc tgg gaa gaa ggc ccc aac agc ttc cag cct tct gat cca atg 384

103 Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met

104 115 120 125

105 ctc acc atg gtg gtg gac agt ggt tta aag gat gag ctt gtt ttg ggg 432

106 Leu Thr Met Val Val Asp Ser Gly Leu Lys Asp Glu Leu Val Leu Gly

107 130 135 140

108 gat cct gat gca cct ccg ttt gtg ttg tgg aac agg aag ttg agg ccg 480

109 Asp Pro Asp Ala Pro Arg Phe Val Leu Trp Asn Arg Lys Leu Arg Pro

110 145 150 155 160

111 gtg ccc ggg aag ctg act gat ttg cct ttc ttt gac ttg atg agc att 528

112 Val Pro Gly Lys Leu Thr Asp Leu Pro Phe Phe Asp Leu Met Ser Ile

113 165 170 175

114 ggt ggc aaa atc agg gct ggc ttt ggt gcg ctt gga att ccg cct cct 576

115 Gly Gly Lys Ile Arg Ala Gly Phe Gly Ala Leu Gly Ile Arg Pro Pro

116 180 185 190

117 cct cca ggt cat gag gaa tcg gtt gaa gag ttt gtt cgt ccg aac ctt 624

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Input Set : A:\0020-4764P.st25A.txt

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118	Pro	Pro	Gly	His	Glu	Glu	Ser	Val	Glu	Glu	Phe	Val	Arg	Arg	Asn	Leu	
119			195					200					205				
120	ggt	gat	gag	gtt	ttt	gaa	cgg	ttg	ata	gag	cct	ttt	tgt	tca	ggg	gtc	672
121	Gly	Asp	Glu	Val	Phe	Glu	Arg	Leu	Ile	Glu	Pro	Phe	Cys	Ser	Gly	Val	
122			210					215				220					
123	tat	gca	ggc	gat	cct	tca	aaa	tta	agt	atg	aaa	gca	gca	ttc	ggg	aaa	720
124	Tyr	Ala	Gly	Asp	Pro	Ser	Lys	Leu	Ser	Met	Lys	Ala	Ala	Phe	Gly	Lys	
125	225							230				235				240	
126	gtt	tgg	aag	ctg	gaa	aaa	aat	ggt	ggt	agc	att	att	ggt	gga	act	ttc	768
127	Val	Trp	Lys	Leu	Glu	Lys	Asn	Gly	Gly	Ser	Ile	Ile	Gly	Gly	Thr	Phe	
128					245					250					255		
129	aaa	gca	ata	caa	gag	aga	aat	gga	gct	tca	aaa	cca	cct	cga	gat	ccg	816
130	Lys	Ala	Ile	Gln	Glu	Arg	Asn	Gly	Ala	Ser	Lys	Pro	Pro	Arg	Asp	Pro	
131				260						265					270		
132	cgt	ctg	cca	aaa	cca	aaa	ggt	cag	act	gtt	gga	tct	ttc	cgg	aag	gga	864
133	Arg	Leu	Pro	Lys	Pro	Lys	Gly	Gln	Thr	Val	Gly	Ser	Phe	Arg	Lys	Gly	
134			275					280					285				
135	ctt	acc	atg	ttg	cct	gat	gca	att	tct	gcc	aga	cta	ggc	aac	aaa	gta	912
136	Leu	Thr	Met	Leu	Pro	Asp	Ala	Ile	Ser	Ala	Arg	Leu	Gly	Asn	Lys	Val	
137			290					295				300					
138	aag	tta	tct	tgg	aag	ctt	tca	agt	att	agt	aaa	ctg	gat	agt	gga	gag	960
139	Lys	Leu	Ser	Trp	Lys	Leu	Ser	Ser	Ile	Ser	Lys	Leu	Asp	Ser	Gly	Glu	
140	305					310					315					320	
141	tac	agt	ttg	aca	tat	gaa	aca	cca	gaa	gga	gtg	gtt	tct	ttg	cag	tgc	1008
142	Tyr	Ser	Leu	Thr	Tyr	Glu	Thr	Pro	Glu	Gly	Val	Val	Ser	Leu	Gln	Cys	
143					325						330				335		
144	aaa	act	gtt	gtc	ctg	acc	att	cct	tcc	tat	gtt	gct	agt	aca	ttg	ctg	1056
145	Lys	Thr	Val	Val	Leu	Thr	Ile	Pro	Ser	Tyr	Val	Ala	Ser	Thr	Leu	Leu	
146				340						345				350			
147	cgt	cct	ctg	tct	gct	gct	gct	gca	gat	gca	ctt	tca	aag	ttt	tat	tac	1104
148	Arg	Pro	Leu	Ser	Ala	Ala	Ala	Ala	Asp	Ala	Leu	Ser	Lys	Phe	Tyr	Tyr	
149			355					360					365				
150	cct	cca	gtt	gct	gca	gtt	tcc	ata	tcc	tat	cca	aaa	gaa	gct	att	aga	1152
151	Pro	Pro	Val	Ala	Ala	Val	Ser	Ile	Ser	Tyr	Pro	Lys	Glu	Ala	Ile	Arg	
152			370					375				380					
153	tca	gaa	tgc	ttg	ata	gat	ggt	gag	ttg	aag	ggg	ttt	ggt	caa	ttg	cat	1200
154	Ser	Glu	Cys	Leu	Ile	Asp	Gly	Glu	Leu	Lys	Gly	Phe	Gly	Gln	Leu	His	
155	385					390					395				400		
156	cca	cgt	agc	caa	gga	gtg	gaa	aca	tta	gga	act	ata	tac	agc	tca	tca	1248
157	Pro	Arg	Ser	Gln	Gly	Val	Glu	Thr	Leu	Gly	Thr	Ile	Tyr	Ser	Ser	Ser	
158					405					410					415		
159	cta	ttc	ccc	aac	cga	gca	cca	cct	gga	agg	gtt	cta	ctc	ttg	aat	tac	1296
160	Leu	Phe	Pro	Asn	Arg	Ala	Pro	Pro	Gly	Arg	Val	Leu	Leu	Leu	Asn	Tyr	
161				420					425						430		
162	att	gga	gga	gca	act	aat	act	gga	att	tta	tcg	aag	acg	gac	agt	gaa	1344
163	Ile	Gly	Gly	Ala	Thr	Asn	Thr	Gly	Ile	Leu	Ser	Lys	Thr	Asp	Ser	Glu	
164			435					440					445				
165	ctt	gtg	gaa	aca	gtt	gat	cga	gat	ttg	agg	aaa	atc	ctt	ata	aac	cca	1392
166	Leu	Val	Glu	Thr	Val	Asp	Arg	Asp	Leu	Arg	Lys	Ile	Leu	Ile	Asn	Pro	

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167      450      455      460
168 aat gcc cag gat cca ttt gta gtg ggg gtg aga ctg tgg cct caa gct 1440
169 Asn Ala Gln Asp Pro Phe Val Val Gly Val Arg Leu Trp Pro Gln Ala
170 465      470      475      480
171 att cca cag ttc tta gtt ggc cat ctt gat ctt cta gat gtt gct aaa 1488
172 Ile Pro Gln Phe Leu Val Gly His Leu Asp Leu Leu Asp Val Ala Lys
173      485      490      495
174 gct tct atc aga aat act ggg ttt gaa ggg ctc ttc ctt ggg ggt aat 1536
175 Ala Ser Ile Arg Asn Thr Gly Phe Glu Gly Leu Phe Leu Gly Gly Asn
176      500      505      510
177 tat gtg tct ggt gtt gcc ttg gga cga tgc gtt gag gga gcc tat gag 1584
178 Tyr Val Ser Gly Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu
179      515      520      525
180 gta gca gct gaa gta aac gat ttt ctc aca aat aga gtg tac aaa tag 1632
181 Val Ala Ala Glu Val Asn Asp Phe Leu Thr Asn Arg Val Tyr Lys
182      530      535      540      543
184 <210> SEQ ID NO: 6
185 <211> LENGTH: 543
186 <212> TYPE: PRT
187 <213> ORGANISM: Glycine max var. Williams82
189 <400> SEQUENCE: 6
190 Met Val Ser Val Phe Asn Glu Ile Leu Phe Pro Pro Asn Gln Thr Leu
191 1      5      10      15
192 Leu Arg Pro Ser Leu His Ser Pro Thr Ser Phe Phe Thr Ser Pro Thr
193      20      25      30
194 Arg Lys Phe Pro Arg Ser Arg Pro Asn Pro Ile Leu Arg Cys Ser Ile
195      35      40      45
196 Ala Glu Glu Ser Thr Ala Ser Pro Pro Lys Thr Arg Asp Ser Ala Pro
197      50      55      60
198 Val Asp Cys Val Val Val Gly Gly Gly Val Ser Gly Leu Cys Ile Ala
199 65      70      75      80
200 Gln Ala Leu Ala Thr Lys His Ala Asn Ala Asn Val Val Val Thr Glu
201      85      90      95
202 Ala Arg Asp Arg Val Gly Gly Asn Ile Thr Thr Met Glu Arg Asp Gly
203      100      105      110
204 Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met
205      115      120      125
206 Leu Thr Met Val Val Asp Ser Gly Leu Lys Asp Glu Leu Val Leu Gly
207      130      135      140
208 Asp Pro Asp Ala Pro Arg Phe Val Leu Trp Asn Arg Lys Leu Arg Pro
209 145      150      155      160
210 Val Pro Gly Lys Leu Thr Asp Leu Pro Phe Phe Asp Leu Met Ser Ile
211      165      170      175
212 Gly Gly Lys Ile Arg Ala Gly Phe Gly Ala Leu Gly Ile Arg Pro Pro
213      180      185      190
214 Pro Pro Gly His Glu Glu Ser Val Glu Glu Phe Val Arg Arg Asn Leu
215      195      200      205
216 Gly Asp Glu Val Phe Glu Arg Leu Ile Glu Pro Phe Cys Ser Gly Val
217      210      215      220

```

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```

218 Tyr Ala Gly Asp Pro Ser Lys Leu Ser Met Lys Ala Ala Phe Gly Lys
219 225                230                235                240
220 Val Trp Lys Leu Glu Lys Asn Gly Gly Ser Ile Ile Gly Gly Thr Phe
221                245                250                255
222 Lys Ala Ile Gln Glu Arg Asn Gly Ala Ser Lys Pro Pro Arg Asp Pro
223                260                265                270
224 Arg Leu Pro Lys Pro Lys Gly Gln Thr Val Gly Ser Phe Arg Lys Gly
225                275                280                285
226 Leu Thr Met Leu Pro Asp Ala Ile Ser Ala Arg Leu Gly Asn Lys Val
227                290                295                300
228 Lys Leu Ser Trp Lys Leu Ser Ser Ile Ser Lys Leu Asp Ser Gly Glu
229 305                310                315                320
230 Tyr Ser Leu Thr Tyr Glu Thr Pro Glu Gly Val Val Ser Leu Gln Cys
231                325                330                335
232 Lys Thr Val Val Leu Thr Ile Pro Ser Tyr Val Ala Ser Thr Leu Leu
233                340                345                350
234 Arg Pro Leu Ser Ala Ala Ala Ala Asp Ala Leu Ser Lys Phe Tyr Tyr
235                355                360                365
236 Pro Pro Val Ala Ala Val Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg
237                370                375                380
238 Ser Glu Cys Leu Ile Asp Gly Glu Leu Lys Gly Phe Gly Gln Leu His
239 385                390                395                400
240 Pro Arg Ser Gln Gly Val Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser
241                405                410                415
242 Leu Phe Pro Asn Arg Ala Pro Pro Gly Arg Val Leu Leu Leu Asn Tyr
243                420                425                430
244 Ile Gly Gly Ala Thr Asn Thr Gly Ile Leu Ser Lys Thr Asp Ser Glu
245                435                440                445
246 Leu Val Glu Thr Val Asp Arg Asp Leu Arg Lys Ile Leu Ile Asn Pro
247                450                455                460
248 Asn Ala Gln Asp Pro Phe Val Val Gly Val Arg Leu Trp Pro Gln Ala
249 465                470                475                480
250 Ile Pro Gln Phe Leu Val Gly His Leu Asp Leu Leu Asp Val Ala Lys
251                485                490                495
252 Ala Ser Ile Arg Asn Thr Gly Phe Glu Gly Leu Phe Leu Gly Gly Asn
253                500                505                510
254 Tyr Val Ser Gly Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu
255                515                520                525
256 Val Ala Ala Glu Val Asn Asp Phe Leu Thr Asn Arg Val Tyr Lys
257                530                535                540                543
259 <210> SEQ ID NO: 7
260 <211> LENGTH: 39
261 <212> TYPE: DNA
262 <213> ORGANISM: Artificial Sequence
264 <220> FEATURE:
265 <223> OTHER INFORMATION: Designed oligonucleotide primer to amplify bchH gene
267 <400> SEQUENCE: 7
268 gacatctagt ctagacgacc atatgcacgg tgaagtctc      39
270 <210> SEQ ID NO: 8

```

RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:27; N Pos. 6,7,9,10,12,13,15,16,18,19  
Seq#:28; N Pos. 8,9,11,12,14,15,17,18,20,21  
Seq#:77; Xaa Pos. 2,4,5

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:9; Line(s) 287  
Seq#:10; Line(s) 298  
Seq#:11; Line(s) 309  
Seq#:12; Line(s) 320  
Seq#:13; Line(s) 331  
Seq#:14; Line(s) 342  
Seq#:19; Line(s) 576  
Seq#:20; Line(s) 587  
Seq#:21; Line(s) 598  
Seq#:22; Line(s) 609  
Seq#:27; Line(s) 664  
Seq#:28; Line(s) 680  
Seq#:29; Line(s) 696  
Seq#:30; Line(s) 707  
Seq#:31; Line(s) 718  
Seq#:32; Line(s) 729  
Seq#:33; Line(s) 740  
Seq#:34; Line(s) 751  
Seq#:35; Line(s) 762  
Seq#:36; Line(s) 773  
Seq#:37; Line(s) 784  
Seq#:38; Line(s) 795  
Seq#:39; Line(s) 806  
Seq#:40; Line(s) 817  
Seq#:41; Line(s) 828  
Seq#:42; Line(s) 839  
Seq#:43; Line(s) 850  
Seq#:44; Line(s) 861  
Seq#:45; Line(s) 872  
Seq#:46; Line(s) 883  
Seq#:47; Line(s) 894  
Seq#:48; Line(s) 905  
Seq#:49; Line(s) 916  
Seq#:50; Line(s) 927  
Seq#:51; Line(s) 938  
Seq#:52; Line(s) 949